

OIPF

RAW SEQUENCE LISTING

DATE: 11/26/2001

PATENT APPLICATION: US/09/919,831

TIME: 15:04:22

Input Set : A:\211736US0X.txt

Output Set: N:\CRF3\11212001\I919831.raw

ENTERED

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3 <110> APPLICANT: BATHE, BRIGITTE
4   PFEFFERLE, WALTER
5   HUTHMACHER, KLAUS
6   RUECKERT, CHRISTIAN
7   KALINOWSKI, JOERN
8   PUEHLER, ALFRED
9   BINDER, MICHAEL
10  GREISSINGER, DIETER
11  IHIERBACH, GEORG
13 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METR AND METZ GENES
15 <130> FILE REFERENCE: 211736US0X
17 <140> CURRENT APPLICATION NUMBER: 09/919,831
18 <141> CURRENT FILING DATE: 2001-08-02
20 <150> PRIOR APPLICATION NUMBER: DE 10043335.9
21 <151> PRIOR FILING DATE: 2000-09-02
23 <150> PRIOR APPLICATION NUMBER: DE 10109688.7
24 <151> PRIOR FILING DATE: 2001-02-28
26 <160> NUMBER OF SEQ ID NOS: 8
28 <170> SOFTWARE: PatentIn version 3.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2628
32 <212> TYPE: DNA
33 <213> ORGANISM: Corynebacterium glutamicum
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36 <221> NAME/KEY: CDS
37 <222> LOCATION: (447)..(1013)
38 <223> OTHER INFORMATION:
41 <220> FEATURE:
42 <221> NAME/KEY: CDS
43 <222> LOCATION: (1038)..(2183)
44 <223> OTHER INFORMATION:
47 <400> SEQUENCE: 1
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50 ttttcggggg aactgaaaaa catcgtcgga taggcagcgc tataattcag cagcgatttc      120
52 ggcagcaagc ccagcgccat taatcagagc ggtgaaataa acatggttca tgattatgtc      180
54 aggaacggtaa ttagacttat gaccaggttt aaggaggtea ccaggttgaa gccgcgctat      240
56 tgttcggtg aaaagggggc cctgatctag ctgattattc atcgcagtaa gcgctttcgg      300
58 taggtgggtg aatcctcgta gtcttcgag ccccgtagcc cgatecgttt tgtgcaatcc      360
60 aatgctactc ccacagagcg ggctactttc tctaaaaatg ttctcatagt agataaaatt      420
62 gttcttaaag cgacattatt gtctgc atg gaa gac gat ctc agt gct gct ctc      473
63                               Met Glu Asp Asp Leu Ser Ala Ala Leu
64                               1           5
66 gtc aaa gcg ctt ttc gac gcg cga acc caa cgc agg ctc tct atc tcg      521
                               Met Thr Thr Thr Thr Arg Arg Leu Ser Ile Ser

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72	30	35	40	
74	gaa aac gca gag gcg caa cca agc gct gca tta ctt gga cgc ctt tcc	617		
75	Glu Asn Ala Glu Ala Gln Pro Ser Ala Ala Leu Leu Gly Arg Leu Ser			
76	45 50 55			
78	ggt gca ttg ggt atg acg ctt tgg gag ctc att gca cag gct gaa ggt	665		
79	Gly Ala Leu Gly Met Thr Leu Ser Glu Leu Ile Ala Gln Ala Glu Gly			
80	60 65 70			
82	ggc tat gac cgg ggc gct cgg cgg tca aag cag tct gta tgg aca gat	713		
83	Gly Tyr Asp Arg Gly Ala Arg Arg Ser Lys Gln Ser Val Trp Thr Asp			
84	75 80 85			
86	cca gct acc ggt tac aca cgg cgt gca gtg tca cag ccg tca gaa tcc	761		
87	Pro Ala Thr Gly Tyr Thr Arg Arg Ala Val Ser Gln Pro Ser Glu Ser			
88	90 95 100 105			
90	cca cta gaa cta gtg gaa gta atg ctg cct cct ggg gcg gaa gtt ggc	809		
91	Pro Leu Glu Leu Val Glu Val Met Leu Pro Pro Gly Ala Glu Val Gly			
92	110 115 120			
94	tac cca gct gat gct tat cgt ttc atg gat cag gly gtc tgg gta ctc	857		
95	Tyr Pro Ala Asp Ala Tyr Arg Phe Met Asp Gln Val Val Trp Val Leu			
96	125 130 135			
98	gaa ggg gcc gtt cgt att act gaa ggt gaa gag gtc cac gaa ctt tca	905		
99	Glu Gly Ala Val Arg Ile Thr Glu Gly Glu Glu Val His Glu Leu Ser			
100	140 145 150			
102	acg ggg gat tgt cta cgg ttt ggg cct ccg cga gat acc gac ttt gct	953		
103	Thr Gly Asp Cys Leu Arg Phe Gly Pro Pro Arg Asp Thr Asp Phe Ala			
104	155 160 165			
106	aat ccc acc acc gta gcc act agg tat tta gtt gcc ttg gac aag cgt	1001		
107	Asn Pro Thr Thr Val Ala Thr Arg Tyr Leu Val Ala Leu Asp Lys Arg			
108	170 175 180 185			
110	gta cct cgt gct tgatataaca agtaaggaag cctg atg aat ttt tac cca	1052		
111	Val Pro Arg Ala Met Asn Phe Tyr Pro			
112	190			
114	cca tct gta cct att aac cct gcg tgg cgt cca ccc aca gta act gtg	1100		
115	Pro Ser Val Pro Ile Asn Pro Ala Trp Arg Pro Pro Thr Val Thr Val			
116	195 200 205 210			
118	caa gcg gga cgg cca gcc aga act cct ggt gcg ccg atg aac cca cct	1148		
119	Gln Ala Gly Arg Pro Ala Arg Thr Pro Gly Ala Pro Met Asn Pro Pro			
120	215 220 225			
122	atc acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg	1196		
123	Ile Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu Lys Ala Tyr Gly			
124	230 235 240			
126	cgc gat gcc aat gat qga tgg qgt gca ttt gag gct gcc atg gga act	1244		
127	Arg Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala Ala Met Gly Thr			
128	245 250 255			
130	cta gat ggt ggg ttc gcg gta tct tat tct tca ggt ttg gca gcg gca	1292		
131	Leu Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly Leu Ala Ala Ala			
132	260 265 270			
134	acg tgg att gct gat ttg gtt cct act ggt ggc aca gtt gtt tta cct	1340		
135	Thr Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr Val Val Leu Pro			

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138 aaa gct gcc tat tat ggc gtg acc aat att ttc gcc agg atg gaa gcc      1388
139 Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala Arg Met Glu Ala
140          295          300          305
142 cgc gga agg ctg aag gtt cga act gtt gat gca gac aat acc gaa gaa      1436
143 Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp Asn Thr Glu Glu
144          310          315          320
146 gtg att gct gct gct caa ggt gca gat gtg gtg tgg gtg gaa tcg atc      1484
147 Val Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp Val Glu Ser Ile
148          325          330          335
150 gct aat ccg acg atg gtg gta gct gat atc cct gca ata gtc gac ggt      1532
151 Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala Ile Val Asp Gly
152          340          345          350
154 gtg cgt ggg ctt gga gtt ttg act gtc gtt gac gcg act ttc gca acg      1580
155 Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala Thr Phe Ala Thr
156 355          360          365          370
158 cca ctt cgt caa cgt cca ttg gaa ctt ggt gat att gtg ctt tac      1628
159 Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp Ile Val Leu Tyr
160          375          380          385
162 tcg gca acc aaa ctt atc ggt gga cac tct gat ctt ctt ctt gga gtc      1676
163 Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu Leu Leu Gly Val
164          390          395          400
166 gca gtg tgc aag tct gag cac cat gcg cag ttt ctt gcc act cac cgt      1724
167 Ala Val Cys Lys Ser Glu His His Ala Gln Phe Leu Ala Thr His Arg
168          405          410          415
170 cat gat cat ggt tca gtg ccg gga ggt ctt gaa gcg ttt ctt gct ctc      1772
171 His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala Phe Leu Ala Leu
172          420          425          430
174 cgt gga ttg tat tcc ttg gcg gtg cgt ctt gat cga gca gaa tcc aac      1820
175 Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg Ala Glu Ser Asn
176 435          440          445          450
178 gca gca gaa ctt tcg cgg cga ctt aac gcg cat cct tcg gtt acc cgc      1868
179 Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro Ser Val Thr Arg
180          455          460          465
182 gtc aat tat cca gga ctt cct gat gat ccc caa cat gaa aaa gcc gtg      1916
183 Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His Glu Lys Ala Val
184          470          475          480
186 cga gtc cta ccc tct gga tgt gga aac atg ttg tca ttt gag ctt gat      1964
187 Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser Phe Glu Leu Asp
188          485          490          495
190 gca aca cct gaa cga act gat gag att ctc gaa agc ctg tca ctt tta      2012
191 Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser Leu Ser Leu Leu
192          500          505          510
194 acc cac gcg acc agt tgg gga ggt gtg gaa aca gcc att gaa cgt cgc      2060
195 Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala Ile Glu Arg Arg
196 515          520          525          530
198 acc aag cgg gat gct gaa gtg gtg gca gga gta ccg atg act ctt tgc      2108
199 Thr Arg Arg Asp Ala Glu Val Val Ala Gly Val Pro Met Thr Leu Cys
200          535          540          545

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203 Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu Trp Glu Asp Leu
204          550          555          560
206 aac gcc tca atc gac aaa gtt ctg ggt tagaactcgt agccagtaac      2203
207 Asn Ala Ser Ile Asp Lys Val Leu Gly
208          565          570
210 cagaccttca gtgtttggtt gccactccag tgetggggcg acatgatcag cgaagttctt      2263
212 caggatcgac gcgttgatct caacacccat ttggttgggg gcggtgagca tcaagggtgc      2323
214 ggcttccatc acagctttgt cttccttgag ctggtcgatg agttcatcgg gacttccggc      2383
216 gtagctgcga ccgaacgtgg atcgggtatc atccaggatt cctacttggg caccgccttg      2443
218 tccctgaagt ccgaaaagct caccgtcgcg gtcggtgacg atcggaaga tggacctgga      2503
220 gacagacaca cgtgggggtc aatcgtgtcc ggcttcttcc caagcttggc ggtagaacgc      2563
222 gatttgatcg gcttgcatat ccccgaaagga ttggccggtg gcttcggcga cgagggtgga      2623
224 gctca      2628
227 <210> SEQ ID NO: 2
228 <211> LENGTH: 189
229 <212> TYPE: PRT
230 <213> ORGANISM: Corynebacterium glutamicum
232 <400> SEQUENCE: 2
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235 1          5          10          15
238 Arg Thr Gln Arg Arg Leu Ser Ile Ser Ala Leu Ala Glu Ser Ser Gly
239          20          25          30
242 Val Ser Arg Ala Met Ile Ser Arg Val Glu Asn Ala Glu Ala Gln Pro
243          35          40          45
246 Ser Ala Ala Leu Leu Gly Arg Leu Ser Gly Ala Leu Gly Met Thr Leu
247          50          55          60
250 Ser Glu Leu Ile Ala Gln Ala Glu Gly Gly Tyr Asp Arg Gly Ala Arg
251 65          70          75          80
254 Arg Ser Lys Gln Ser Val Trp Thr Asp Pro Ala Thr Gly Tyr Thr Arg
255          85          90          95
258 Arg Ala Val Ser Gln Pro Ser Glu Ser Pro Leu Glu Leu Val Glu Val
259          100          105          110
262 Met Leu Pro Pro Gly Ala Glu Val Gly Tyr Pro Ala Asp Ala Tyr Arg
263          115          120          125
266 Phe Met Asp Gln Val Val Trp Val Leu Glu Gly Ala Val Arg Ile Thr
267          130          135          140
270 Glu Gly Glu Glu Val His Glu Leu Ser Thr Gly Asp Cys Leu Arg Phe
271 145          150          155          160
274 Gly Pro Pro Arg Asp Thr Asp Phe Ala Asn Pro Thr Thr Val Ala Thr
275          165          170          175
278 Arg Tyr Leu Val Ala Leu Asp Lys Arg Val Pro Arg Ala
279          180          185
282 <210> SEQ ID NO: 3
283 <211> LENGTH: 382
284 <212> TYPE: PRT
285 <213> ORGANISM: Corynebacterium glutamicum
287 <400> SEQUENCE: 3
289 Met Asn Phe Tyr Pro Pro Ser Val Pro Ile Asn Pro Ala Trp Arg Pro

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293 Pro Thr Val Thr Val Gln Ala Gly Arg Pro Ala Arg Thr Pro Gly Ala
294          20          25          30
297 Pro Met Asn Pro Pro Ile Thr Leu Ser Ser Thr Tyr Val His Asp Ser
298          35          40          45
301 Glu Lys Ala Tyr Gly Arg Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu
302          50          55          60
305 Ala Ala Met Gly Thr Leu Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser
306 65          70          75          80
309 Gly Leu Ala Ala Ala Thr Ser Ile Ala Asp Leu Val Pro Thr Gly Gly
310          85          90          95
313 Thr Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe
314          100         105         110
317 Ala Arg Met Glu Ala Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala
318          115         120         125
321 Asp Asn Thr Glu Glu Val Ile Ala Ala Ala Gln Gly Ala Asp Val Val
322          130         135         140
325 Trp Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro
326 145         150         155         160
329 Ala Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp
330          165         170         175
333 Ala Thr Phe Ala Thr Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala
334          180         185         190
337 Asp Ile Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp
338          195         200         205
341 Leu Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Gln Phe
342          210         215         220
345 Leu Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu
346 225         230         235         240
349 Ala Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp
350          245         250         255
353 Arg Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His
354          260         265         270
357 Pro Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln
358          275         280         285
361 His Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu
362          290         295         300
365 Ser Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu
366 305         310         315         320
369 Ser Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr
370          325         330         335
373 Ala Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Gly Val
374          340         345         350
377 Pro Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp
378          355         360         365
381 Leu Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly
382          370         375         380
385 <210> SEQ ID NO: 4
386 <211> LENGTH: 32

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VERIFICATION SUMMARY

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